

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 15, 2002, 07:03:49 ; Search time 62.04 Seconds  
(without alignments)  
1275.521 Million cell updates/sec

Title: US-09-652-292-2  
Perfect score: 2765  
Sequence: 1 MCHSPVLPCLASVSLGLG.....GHRQNSTGIPYSRIEISAAS 541

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL17.\*  
1: sp\_archea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2765	100.0	541	4	O95528
2	932	33.7	621	6	O9BE72
3	626.5	22.7	457	2	P96742
4	594.5	21.5	580	10	O9C757
5	575	20.8	558	10	O9F1F2
6	569.5	20.6	502	10	O9FRP7
7	567	20.5	521	10	O22848
8	545	19.7	580	10	O9ZQP6
9	541	19.6	582	10	O23492
10	529	19.1	574	10	O9AUM9
11	529	19.1	581	10	O9LKH2
12	526.5	19.0	581	10	O9LKH1
13	521.5	18.9	433	2	O9CFH3
14	519	18.8	534	10	O9LLE1
15	516	18.7	470	10	O9LLE0
16	515	18.6	555	10	O9FXV8
17	508	18.4	493	10	O23213
18	507	18.3	551	10	O9LLE2
19	502	18.2	515	10	O9LLE8

20	497	18.0	511	10	O9XIH6
21	497	18.0	606	5	O9XXK3
22	495.5	17.9	539	10	O9LS92
23	495	17.9	560	10	O9LF13
24	491.5	17.8	542	10	O9LLD9
25	491	17.8	473	2	O05182
26	491	17.8	523	10	O06312
27	488.5	17.7	464	2	P96710
28	488.5	17.7	522	10	O9SXB1
29	488	17.6	519	10	O9ZS76
30	485.5	17.6	479	2	O9FDM0
31	484.5	17.5	511	10	O9XIH7
32	483	17.5	516	10	O04078
33	482.5	17.5	513	10	O9FOX3
34	482	17.4	508	10	O65413
35	480.5	17.4	545	10	P93076
36	480.5	17.4	549	10	P93075
37	480	17.4	477	4	O9NSC4
38	475	17.2	519	10	O9Z863
39	474.5	17.2	478	11	O9JJ21
40	472	17.1	479	11	O9JMA6
41	471.5	17.1	510	10	O65322
42	471.5	17.1	639	5	O21455
43	470	17.0	470	2	O9KJY1
44	470	17.0	477	4	O9NY64
45	468	16.9	475	10	O48537

## ALIGNMENTS

## RESULT 1

O95528 PRELIMINARY: PRT: 541 AA.  
 AC O95528; O9H416;  
 DT 01-MAY-1999 (TRENBLrel. 10, Created)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
 DE OJ28H20.1 (SOLUTE CARRIER FAMILY 2 (FACILITATED GLUCOSE TRANSPORTER), MEMBER 10) (HYPOTHETICAL 56.9 KDA PROTEIN) (FACILITATIVE GLUCOSE TRANSPORTER GLUT10).  
 DE TRANSPORTER GLUT10.  
 GN SLC2A10 OR GLUT10.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ramsay.H.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Stavrides G.S., Hashim Y., Huckle E.J., Deloukas P.;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Fossey S.C., Mihic S.J., Craddock A.L., Mychalecky J.C., Dawson P.A., Bowden D.W.;  
 RT \*GLUT10: A novel glucose transporter in the type 2 diabetes linked region of chromosome 20q12-13.1.\*;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21145593; PubMed=11247674;  
 RA McVie-Wylie A.J., Lamson D.R., Chen Y.T.;  
 RT "Molecular Cloning of a Novel Member of the GLUT Family of Transporters, SLC2A10 (GLUT10), Localized on Chromosome 20q13.1: A Candidate Gene for NIDDM Susceptibility.\*";  
 RL Genomics 72:113-117(2001).  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -!- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.  
 DR EMBL; AL031055; CAA19926.2; -.  
 DR EMBL; AL137188; CAB69822.2; -.

O9XIH6 arabidopsis  
 O9XIR3 caenorhabdi  
 O9IS92 arabidopsis  
 O9LF13 arabidopsis  
 O9LID9 zea mays (m  
 O05182 bacillus me  
 O06312 nicotiana t  
 P96710 bacillus su  
 O9SXB1 arabidopsis  
 O9ZS76 vitis vinif  
 O9FDM0 zymomonas m  
 O9XIH7 arabidopsis  
 O04078 vicia faba  
 O9FQX3 apium grave  
 O65413 arabidopsis  
 P93076 beta vulgar  
 P93075 beta vulgar  
 O9NSC4 homo sapien  
 O9Z863 vitis vinif  
 O9JJ21 rattus norv  
 O9JMA6 rattus norv  
 O65322 petunia hyb  
 O21455 caenorhabdi  
 O9KJY1 lactobacill  
 O9NY64 homo sapien  
 O48537 prunus arme

DR EMBL; AF248053; AAK31911.1; -  
 DR EMBL; AF321240; AAK26294.1; -  
 DR InterPro: IPR003662; sub.transporter.  
 DR InterPro: IPR003663; sugar\_transporter.  
 DR Pfam: PF00083; sugar\_cr; 1.  
 DR PRINTS; PR00171; SUGTRNSPORT.  
 DR PROSITE; PS00216; SUGAR\_TRANSPORT\_1; UNKNOWN.1.  
 KW Hypothetical protein; Sugar transporter; Transmembrane.  
 SQ SEQUENCE 541 AA; 56911 MW; 6D644525FA136908 CRC64;

Query Match 100.0%; Score 2765; DB 4; Length 541;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-152;  
 Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGHSPVPPLPCASVSLGGLTTCYELAVISGALLPLQDPLGSLCDEQEFVLSGLLIGALL 60  
 DB 1 MGHSPVPPLPCASVSLGGLTTCYELAVISGALLPLQDPLGSLCDEQEFVLSGLLIGALL 60  
 QY 61 ASLVGGFLIDCYGRKQAILGSLNVLGSLTLGLAGSLAWLVGRAVVGFAISLSMACC 120  
 DB 61 ASLVGGFLIDCYGRKQAILGSLNVLGSLTLGLAGSLAWLVGRAVVGFAISLSMACC 120  
 QY 121 IYSELVGPORGVLSVLEAGTTCGILLSYALNYALAGTTPGWRHMFQWATAPAVLQSL 180  
 DB 121 IYSELVGPORGVLSVLEAGTTCGILLSYALNYALAGTTPGWRHMFQWATAPAVLQSL 180  
 QY 181 SLFLPAGTDETHKDLIPLQGGAPKLGPRPRYSFLDLFRANDMRGRTTVGLGLVL 240  
 DB 181 SLFLPAGTDETHKDLIPLQGGAPKLGPRPRYSFLDLFRANDMRGRTTVGLGLVL 240  
 QY 241 FOOLTGPQNVLCYASTIFSSVGFHGGSSAVLASVGLGAVKVAATITAMGLVDRAGRALL 300  
 DB 241 FOOLTGPQNVLCYASTIFSSVGFHGGSSAVLASVGLGAVKVAATITAMGLVDRAGRALL 300  
 QY 301 LAGCALMALSVSGIGLVFAVPMDSGSCLAVPNATGOTGLPGDSGLLODSSLPIPTN 360  
 DB 301 LAGCALMALSVSGIGLVFAVPMDSGSCLAVPNATGOTGLPGDSGLLODSSLPIPTN 360  
 QY 361 EQDREPILSTAKTKPHRSGDPSAPPRALSSALPGPPLPARGHALLRWALLCLWV 420  
 DB 361 EQDREPILSTAKTKPHRSGDPSAPPRALSSALPGPPLPARGHALLRWALLCLWV 420  
 QY 421 SAFSFGFGVTVLWVLSVPEIRGAFACNSFNWAAANLFLISFLDICTIGLSWTF 480  
 DB 421 SAFSFGFGVTVLWVLSVPEIRGAFACNSFNWAAANLFLISFLDICTIGLSWTF 480  
 QY 481 LVGLTAVLGLGYLYLVFVETKQSLAEIDQFQKRRTLSFGHRONSTGIPYSRIEISAA 540  
 DB 481 LVGLTAVLGLGYLYLVFVETKQSLAEIDQFQKRRTLSFGHRONSTGIPYSRIEISAA 540  
 QY 541 S 541  
 DB 541 S 541

RESULT 2  
 Q9BE72 PRELIMINARY; PRT; 621 AA.  
 AC Q9BE72  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE HYPOTHETICAL 67.5 KDA PROTEIN  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=FRONTAL CORTEX;  
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,

RA Suzuki Y., Sugano S., Hashimoto K.;  
 RT "Isolation of full-length cDNA clones from macaque brain cDNA  
 RL libraries";  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB056798; BAB39322.1;  
 KW Hypothetical protein.  
 SQ SEQUENCE 621 AA; 67485 MW; 9E9384A2320AC716 CRC64;

Query Match 33.7%; Score 932; DB 6; Length 621;  
 Best Local Similarity 39.2%; Pred. No. 1.8e-46;  
 Matches 216; Conservative 85; Mismatches 178; Indels 72; Gaps 7;

QY 10 LCASVSLGGLTFGEYELAVISGALLPLQDPLGSLCDEQEFVLSGLLIGALLASVGGFLI 69  
 DB 46 LSSVTAASGLVGVYELGIIISGALLQIKLITLSCHQEOMVVSLLIGALLASVGGVLI 105  
 QY 70 DCYGRKQAILGSLNVLGSLTLGLAGSLAWLVGRAVVGFAISLSMACCIYVSELVGP 129  
 DB 106 DRYGRTAILLSSCILGSLNVLISLSTVTLVIGRIAGVSISSSIATCIVYIAEAPQ 165  
 QY 130 RORGVLVSEYAGITVIGLLSYALNYALAGTTPGWRHMFQWATAPAVLQSLLELPAGT 189  
 DB 166 HRRGLLVSLNLMIVIGILSAVSNVAFANVPHGKNFGLVPLGILQAIAMVFLPSS- 224  
 QY 190 DETATHKDLIPLQGGAPKLGPRPR-----YSFLLDLFRARD 226  
 DB 225 -----PRLVKGQGEAASKV-LGRRLALSDATEELTVIKSSLKDEYQYFMDLFRSKD 277  
 QY 227 NMRGTTVGLGLVLPQQLTGPQNVLCYASTIFSSVGFHGGSSAVLASVGLGAVKVAATLT 286  
 DB 278 NMRTRIMIGLTLVFPVQITGPQNVLCYASTIFSSVGFHGGSSAVLASVGLGAVKVAATLT 337  
 QY 287 AMGLVDRAGRALLLAGCALMALSVSGIGLVFAVPMDSGSCLAVPNATGOTGLPGDSGLLODSSLPIPTN 326  
 DB 338 ATLLVDHVGSRTELCIGSSVMAASLVMTGIVNLNTHMFTNCRSHNSINOSLDESIVG 397  
 QY 327 PSLAVPNATGOTGLPGDSGLLODSSLPIPTN-----PIPTNEDQREPILSTAKTKPHRSGD 383  
 DB 398 PGNLSASNTLRDFKFGTASHRSLSMLPRNDVDRGETTSASLLNAVLSHTEYQIVTDP 457  
 QY 394 SAPPRALSSALPGPPLPARGHALLRWALLCLWVFAVFAFSGFGVTVLWVLSVPEIR 443  
 DB 458 GDVP-----AFLKWLASLLVYAAAFSGIGLGPMPWLVSSEIFPGI 499  
 QY 444 RGAFAFCNSFNWAAANLFLISFLDICTIGLSWTFLLYGLTAVLGLGYLYLVFVETKQ 503  
 DB 500 RGRAMALTSSMNWGINLLISLTLVTDLIGLPMWCVFIITMSLASLLFVVMFIPETKGC 559  
 QY 504 SLAEIDQFQK 514  
 DB 560 SLEQISMELAK 570

RESULT 3  
 P96742 PRELIMINARY; PRT; 457 AA.  
 AC P96742  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE SIMILAR TO METABOLITE TRANSPORT PROTEINS.  
 GN YWYG.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RA Lelong C., Glaser P., Presecan E., Danchin A.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]

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RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=3384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Besieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klearr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serron P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpatra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RA "the complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC CC -1- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
DR EMBL; Z92954; CAB07473.1; -.
DR EMBL; Z99122; CAB15600.1; -.
DR InterPro; IPR001719; Euk_kinase.
DR InterPro; IPR003662; sub_transporter.
DR InterPro; IPR003663; Sugar transporter.
DR Pfam; PF00083; sugar_tr; 1.
DR PRINTS; PR00171; SUGTRNSPORT
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
DR Complete proteome; Transmembrane.
KW SEQUENCE 457 AA; 49192 MW; E688ECE04C8B6EF7 CRC64;
SQ

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Query Match 22.7%; Score 626.5; DB 2; Length 457;  
 Best Local Similarity 30.1%; Pred. No. 6e-29;  
 Matches 160; Conservative 85; Mismatches 179; Indels 107; Gaps 8;

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QY 17 LGGLTFYGVYELAVISCALLPQLDFGLSCLEOEFLVGLSLGLGALLASLVGGFLIDCYGRKO 76
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
15 LGGALYGVDTGVISGAIFLPMKELGNLAFTEGLGVVSSLLVGLGSGAAGKLTDRFGRRK 74
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 77 ATLGNLVLLAGSLTGLGLSLANLVGLAVVGVFAISLSSMACCIYVSELVPGRGVILV 136
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 75 ATMAAALLFCIGGLGVALAPNTGVNVLPRIILGLAVGTSTTIVPLYLSELAPKRGALS 134
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 137 SLYEAGITVGLLSYALNYALAGTTPGWRHMPGWATAPAVLOSLSLLFLP-----ACT 189
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 135 SLNQMLITVGLLSYVNYIFADAE-ANRWMLGLAAVPSLLILGILFMPSPRWLFTNG 193
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 190 DETATKDLPLQOG-----GEAPKLGCPGRPRYSFLDLFRADNMRCRTTVGLGL 238
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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DB 194 EESKAKKILEKLRGTRKDIDQEIHDIKEAKODEG-----GLKELFDPW--VRPALIAGLGL 247
QY 239 VLFQOLTQOPNVLYCASTIFSSVGFHGSASVAVSGVAGVAAATLTAMGLVDRAGRA 298
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 248 AFLOQFICTNTIYYAPKTETNVGF-GNSASILGTVGITGVNVLMTLVAKIIDKGRKP 306
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 299 LLLACCAALMALSVSGIGLVSPAVPMDSPGSCLAVERNATGOTGLPGDGLQDSSLPPIPR 358
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 307 LLLFNGAGVSLIVLALVNLFF----- 329
QY 359 TNEDQREPLSTAKTKTPHRSPDPSAPPRLASLPGPLPARGHALLRWTALLCLMW 418
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 330 -----NNTFAA-----SMTTVCICLV 345
QY 419 FVSASFSGFGPVTMLVSEIYVEIRGRAFAFCNSFNMAANLFISSLFDLIGTIGLSWT 478
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 346 FIVFVAVSWGPPVWVWMLPFLFPHVRGIGTGVSTLMLHVGTLVSLTYPILMEAGISYL 405
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 479 FLIYGLTAVLGLCFIYLVFPETKSGSLAIFIDQOFKRRFTLSFGHRSNTG 529
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 406 FLIYAAIGIMAFLFVRFKVTETKRSLEIEQDLRDKNGGGAAGKQQTVG 456
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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## RESULT 4

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Q9C757 PRELIMINARY; PRT; 580 AA.
AC Q9C757;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE HYPOTHETICAL 63.4 KDA PROTEIN.
GN F12P21.2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Alcafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaya I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana."
RL Nature 408:816-820(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
DR EMBL; AC073506; AAG50560.1; -.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR InterPro; IPR003662; sub_transporter.
DR InterPro; IPR003663; Sugar transporter.
DR Pfam; PF00083; sugar_tr; 1.
DR PRINTS; PR00171; SUGTRNSPORT.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
KW Hypothetical protein; Transmembrane.
SQ SEQUENCE 580 AA; 63449 MW; B8E03518F05EED79 CRC64;

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Query Match 21.5%; Score 594.5; DB 10; Length 580;  
Best Local Similarity 29.6%; Pred. No. 5.5e-27;  
Matches 173; Conservative 94; Mismatches 217; Indels 101; Gaps 16;

Qy 4 SPVPLPCASVLLGGTFFGYELAVISGALLPQLDF---CLSCLEOFFIVGSLLLGALL 60  
:  
Db 25 NPYVLRLAFSAG-TGLLFGYDTGVVISGALLYIRKDFKSDVRNTWLOBMIVSMVAQAIV 83  
:  
Qy 61 ASLVGFLIDCYGRKQATILGSNLVLLAGSLFTLGAGLSLAWLTVGRVVGFSAISSMACC 120  
:  
Db 84 GAATGGWANDKLGRSATLMADFLLCALITMAAANPSLLVVGVRVFLGVGNASMTAP 143  
:  
Qy 121 IYVELVCPRGORGLVLSIYEAGIVGILLSVALNYALAGTPGWHRHFGWTAPAVLOS 180  
:  
Db 144 LYISEAPAKIRGALVSNGFLITGGOFLSYLINLAFTDVTGTWRMLGIAGIPALLQFV 203  
:  
Qy 181 SLLFLP-----AGTDETA-----THKDLP---LQQGEAPKIGP 211  
:  
Db 204 LMFTLPESPRWLRYKRREEEAKALRRIYSAEVDVEQETRAALKDSVFTEILLEGSSEKI-- 261  
:  
Qy 212 GRPRYSFLDLFRARDNRRTTVGLVLFOOLTGPQNVLICYASTIFSSVGHGGSAVL 271  
:  
Db 262 -----NMKKCKAKTVARG-LIAGVGQVQFOQFYGINVAYSPTIYVOLGASFASNRALL 315  
:  
Qy 272 ASVGLGAVKVAANTLTAMGLVDRCRRALLAGCALMSLYSGIGLVSFAYPMDSGPCSLA 331  
:  
Db 316 LSLVTAGLNAGFSIIISYIFDIRGRKKLLI-----ISLGV-IISLGI----- 357  
:  
Qy 332 VPNATG-----OTGLPGDSL-----LDSSLPIPTRNEDOREPILSTAKTRP----- 376  
:  
Db 358 ---LTGVFEYAATHAPAISLSLETORFNISCPDYKSAMNTNAMDMCTCLKASSPCGYCS 414  
:  
Qy 377 -----HPRS---GDPSAPP-----RLASSLALPGPLPARGHALLRWALLCLMWFS 421  
:  
Db 415 SPIKEHPGACWISDDSVKDLCHNEENLRWTRGCP-----SNFGNALGLGLYII 465  
:  
Qy 422 AFSPGFGPVTLWLSEIYPVEIRGAFAFCNSFNAAANLFISLFDLICITIGLSWTFLL 481  
:  
Db 466 FFSFGMGTVPWINSEIYPLRFRCIGCGIAATANWNISNLIVAQSFLSTEAGTSWTFLLI 525  
:  
Qy 482 YGLTAVLGLGFIYLFVPETTKGSLAEIDQOQFKRRFTLSFGHQON 526  
:  
Db 526 FGVISVIALLFMVCVPEPKGMPEIEKMLERRMEFKFWKKKS 570  
: :

RESULT 5  
Q9FIF2 PRELIMINARY; PRT; 558 AA.  
AC Q9FIF2 AC  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE SUGAR TRANSPORTER-LIKE PROTEIN.  
OS Arabidopsis thaliana (Mouse-ear cross).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopses.  
NCBI\_TaxId=3702;  
[1]  
SEQUENCE FROM N.A.  
RP STRAIN=COLUMBIA;  
RX MEDLINE=99156233; PubMed=10048488;  
RA Asamizu E., Sato S., Kaneo T., Nakamura Y., Kotani H., Miyajima N.,  
RA Tabata S.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VIII.  
RT Sequence features of the regions of 1,081,958 bp covered by seventeen  
RT physically assigned pl and TAC clones."  
RL DNA Res. 5:379-391(1998).  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC EMBL; AB016890; BAB09770.1; -.  
DR InterPro; IPR003662; sub.transporter.  
DR InterPro; IPR003663; Sugar transporter.

Pfam:	PF00083; sugar_tr; l.
DR	PRINTS; PR00171; SUGRTRNSPORT.
DR	PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
KW	Transmembrane.
SQ	SEQUENCE 558 AA; 59829 MW; CAE26ED800053C85 CRC64;

  

Query Match		20.88; Score 575; DB 10; Length 558;
Best Local Similarity		30.1%; Pred. No. 7.1e-26;
Matches 162; Conservative 77; Mismatches 173; Indels 126; Gaps 10;		

  

QY	17	LGGITFCVELAVISGALLPLQLD-----FGLSCLEQEFVLVSGLLIGALLASLVGGFLI	69
DB	107	LGGLFGFDGTGNTSGATLSLSPALSTTTFNFSPVOLGLVWSGLYGALLGSTSYVGVA	166
QY	70	DCYGRKAIIAGSNILLAGSLTLGLAGSLAWLVLGRAVGVFAISLSMACCIIYVSELVGP	129
DB	167	DFLGRRRRLIAAVALYLGLSLITGCAPDLNILLVGRLLYFGIGLAMHGAFLYAETCP	226
QY	130	RQRGVIVSLYEAGTIVGILLSAYLNALNYALAGTPGWHRMFOWATAPAVLQSLSLFLPA--	187
DB	227	QIRGTLSLSKELFIVLGILLGFVSQIDVVGSGWRMYMGFTPVALLMLGMWSLPASP	286
QY	188	-----GTDETATKHOLIQQGGAPKLGP-----RPXY-----	216
DB	287	RWLRLRAVQCKGOQEYKERAMLAALSRLGRPPCDKISEKLVDVDAVLSVKATYDEKSGG	346
QY	217	SFLDLPRARDNRGRTTVGLVGLVLFQOLTGNPNVLCASTIFSVPFHGSSAVLASVGL	276
DB	347	NFLVEVFG-FNLKA-LFPIGGVLVFOQTGPSLYLAGSILOTAGFSAAADATRVSVII	404
QY	277	GAVKVAATLTAMGLVDNRARRALLAGCALMALSVSGISGLVSFAVPMDSGPCSLAVPNAT	336
DB	405	GVFKLLMTWAVAKVDLGRPLLIG-----VSGIALSLP-----	440
QY	337	GQTGLPGSDGLQDSSLPIPTNEDQREPILTAKTKPKHPSGDPSAPPRIALSSALP	396
DB	441	-----LLS-----YYKFLG	450
QY	397	GPPLPARGHALLRWTALLCLMWVSAPSFSGFPVTWLVLSEIYPVEIRGAFACFSFW	456
DB	451	GFFPLVAVG-----ALLXVGYQTSFGFISLMWSEIFLTRGRGISLAVLTNF	500
QY	457	AANFLSLSLDLIGTITGLSWTEFLXLTAVLGIgfTYLFPVETPKGSGLAEIDQOFK	514
DB	501	GSNAIVTFAFSPLKEFLGAENLFLRGGINALVSLFFVLVVPTKGLSLEIESKILK	558

  

RESULT	6
Q9FRP7	PRELIMINARY; PRT; 502 AA.
AC	Q9FRP7;
DT	01-MAR-2001 (TREMBLrel. 16, Created)
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE	PUTATIVE SUGAR TRANSPORTER PROTEIN.
OS	Oryza sativa (Rice).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	SpERMatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC	Erbartoideae; Oryzaceae; Oryza.
OX	NCBI_TaxId=4530;
RN	[1]
RC	SEQUENCE FROM N.A.
RC	STRAIN=cv. NIPPONBARE;
RA	Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
RA	Zismann V., Pan G., Bowman C.L., Fujii C.Y., VanAken S.E.,
RA	Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblum T.V.,
RA	Quackenbush J., White O., Salzberg S.B., Fraser C.M.;
RT	"Oryza sativa chromosome 10 BAC OSJNBa0056G17 genomic sequence."
RL	Submitted (JAN-2001) to the EMBL/GenBank/DDJB databases.
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC	-!- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
DR	EMBL; AC018727; AAG46179.1; -



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RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.,
RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
RA Fraser C.M., Venter J.C.;
RT "Arabidopsis thaliana chromosome II BAC T20F21 genomic sequence.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
DR EMBL: AC006068; AAD15441.1;
DR Medel; 39574; Arath; 3059; 39574.
DR InterPro: IPR003662; sub_transporter.
DR Pfam: PF00083; sugar_tr; 1.
DR PRINTS: PR00171; SUGTRNSPORT.
DR PROSITE: PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
DR PROSITE: PS00217; SUGAR_TRANSPORT_2; 1.
KW Transmembrane.
SQ SEQUENCE 580 AA; 63171 MW; FC6437FD5A3E00B3 CRC64;

Query Match          19.7%; Score 545; DB 10; Length 580;
Best Local Similarity 28.6%; Pred. No. 4e-24;
Matches 164; Conservative 99; Mismatches 205; Indels 106; Gaps 18;

QY 4 SPVPLPCASVSLGGLTFCGYELAVISGALLPLQLDFG----LSCLEQEFVLGSLLLGALL 60
DB 23 TPYIMRLALSAG-IGGLLFYGTGTAGALLYKEEFGEYDNTKLTQLEIIVSMTVAGAI 81

QY 61 ASLVGGFLIDCYGRKQAILGSLNLVLAGSLTGLAGSLAWLVGRAVGVFAISLSMACC 120
DB 82 GAAIGGWYNDKFGRRMSVLIADVLFLLGLVWVIAHPVILIGRLVLGVGVGMASMTSP 141

QY 121 IYVSELVGPQRGVLSVLEAGITVIGLLSYALNYALAGTTPGWRHMFGWATAPAVLQSL 180
DB 142 LYISESPARIRGALVSTNGLLITGGQFLSYLINLAFVHTPTGWRMLGVSAIPAIQFC 201

QY 181 SLFLPAG-----TDETATKDLI-----PLOGEA-----PKLGPRP 214
DB 202 LMLTLPESPRWLYNRDKAESRDILRIYPAEMVEAEIAALKESVRAETADEIIG---- 257

QY 215 RYSLDLFR-ARDN--MRGRTTVGLGLVLFQOLTGPQNVLCYASTIFSSVGRHGSSAV- 270
DB 258 -HTFSDKLRGALSNPVVRHGLAAGITVQVAQFVGINTVWYSPTLIQFAGVASKNTAMA 316

QY 271 --LASVGLCAVKVAATLTAMGLVDRAGRALLAGCALMALSVSGIGLVFAVPMDSGPS 328
DB 317 LALITSGLNVA--GSVSMFVDRYGRKLMT-----ISMFGII-----T 354

QY 329 CLAVPNATGQTGLPGLDGLDSSLPPIPTNEDQRE-----PILS--TAKTKPH-- 377
DB 355 CLVILAAVFNEA-----SNHAPKIDK--RDSNFKNATCPAFAPFTASRPPSNW 403

QY 378 -----PRSGDPSAPRIALSSALPGPPLPARGHALLR-----WTALLCL 416
DB 404 NCMKLCQYDCGFCNSGAQYAPAGACIVQASDKMALKCHSKGRFTFRDGCPKGYLAIVPL 463

QY 417 MYFVSASFSGFPGVTLVLSLEYVEIRGAPAFCSNFWANLISFLDLITIGLS 476
DB 464 GLYIIVAPGCMGTVPWVNSEIYPLRYRGLAGGIAAVSNMNLVSVSETFLTFLTNAVGS 523

QY 477 WTFLLYGLTAVLGLGFIYLVFPETKQSLAEIDQ 510
DB 524 GFLLFAGSSAVGLFFIWLVPETKGLQFEVEK 557

RESULT 9
O23492 ID O23492 PRELIMINARY; PRT; 582 AA.
AC O23492;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE SIMILARITY TO MEMBRANE TRANSPORT PROTEIN (MEMBRANE TRANSPORTER LIKE

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DE PROTEIN).
GN AT4G16480.
OC Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98121113; PubMed=9461215;
RA Bevan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,
RA Bergkamp R., Dirkse S.A., van Staveren M., Stiekema W., Drost L.,
RA Ridley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H.,
RA Wedler E., Wambutt R., Weitzenecker T., Pohl T.M., Terry N.,
RA Gielen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,
RA Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Funk B., Mueller-Auer S.,
RA Entian K.D., Rieger M., Schaeffer M., Pons A., Puigdomenech P., Douka A.,
RA Silvey M., James R., Montfort A., Hatzopoulos P., Piravandi E., Obermaier B.,
RA Voukelatou E., Milioni D., Hatzopoulos P., Jones J.D.G., Eneva T.,
RA Hilbert H., Duesterhoft A., Moore S., Rechman S., Cooke R., Berger C.,
RA Palme K., Benes V., Voet M., Voickaert G., Mewes H.W., Klosterman S.,
RA Delsen M., Voet M., Voickaert G., Mewes H.W., Klosterman S.,
RA Schueller C., Chaiwatzis N.;
RT "Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of
RT Arabidopsis thaliana.";
RL Nature 391:485-488(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
DR EMBL: 297341; CABL0424.1;
DR EMBL: AL161544; CAB78690.1;
DR Medel; 26756; Arath; 3059; 26756.
DR InterPro: IPR003662; sub_transporter.
DR Pfam: PF00083; sugar_tr; 1.
DR PRINTS: PR00171; SUGTRNSPORT.
DR PROSITE: PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
DR PROSITE: PS00217; SUGAR_TRANSPORT_2; 1.
KW Transmembrane.
SQ SEQUENCE 582 AA; 62891 MW; FA8F8DCA5D0CB0 CRC64;

Query Match          19.6%; Score 541; DB 10; Length 582;
Best Local Similarity 28.8%; Pred. No. 6.8e-24;
Matches 161; Conservative 91; Mismatches 231; Indels 76; Gaps 13;

QY 4 SPVPLPCASVSLGGLTFCGYELAVISGALLPLQLDFG---GLSCLEQEFVLGSLLLGALL 60
DB 24 TPYIMRLALSAG-IGGLLFYGTGTAGALLYKEEFGEYDNTKLTQLEIIVSMTVAGAI 82

QY 61 ASLVGGFLIDCYGRKQAILGSLNLVLAGSLTGLAGSLAWLVGRAVGVFAISLSMACC 120
DB 83 GAAVGGWINDKFGRRMSVLIADVLFLLGLVWVIAHPVILIGRLVLGVGVGMASMTSP 142

QY 121 IYVSELVGPQRGVLSVLEAGITVIGLLSYALNYALAGTTPGWRHMFGWATAPAVLQSL 180
DB 143 LYISESPARIRGALVSTNGLLITGGQFSLYLINLAFVHTPTGWRMLGVSAIPAVQFV 202

QY 181 SLFLPAG-----TDETATKDLIPLQGEAPK-----LGPGR 213
DB 203 LMLSLPESPRWLYNRDKRIAESRAILRIYPADEVAEAEALKL-SVEAKEADEAIIG--- 258

QY 214 PRYFLDLFRAR-----DNMRGRTTVGLGLVLFQOLTGPQNVLCYASTIFSSVGRHG 266
DB 259 -----DSFSAKLKGAFGNPVVRHGLAAGITVQVAQFVGINTVWYSPTLIQFAGV 312

QY 267 SSAVLASVGLCAVKVAATLTAMGLVDRAGRALL-----LAGCALMALSVSGIGLVSA 320
DB 313 KTAMALSITSGLNALGSIIVSMFVDRYGRKLMIIISFGLIACLIILATVFSQAAI-HA 371

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QY 321 VPMDSGPSCLAVPNATGOTGLPGDSSLQDSSLPPIPTNEDQREPIILSTAKKTKPHRPS 380
Db 372 PKIDAFESTFAPNATCSAYAP-----LAAENAPP-----SRWCMKCLRSECGFCAS 419
QY 381 G-DPSAPPRLALSSALPCPLPARGHALLR-----WTALLCLMVFVSFAFSGFGPVT 431
Db 420 GVQYAPGACVVLSDMKATCSSRRTFKDCPKSKFGLAIFVLGLIYVYAPGVTVP 479
QY 432 WLVSVEIYVPEIRAFACFNMAANLFLISLSELDLIGTIGLSWTFLYGLTAVLGLG: 491
Db 480 WIVNSEIYPLRYGLGGGTAASVNVSVNLIVSESLTHALSGSGTELLPAGFTIGLF 539
QY 492 FYLFPVETKGSALAEIQ 510
Db 540 FTWLLVPETKGLQFEVEK 558

RESULT 10
Q9AUM9 PRELIMINARY: PRT: 574 AA.
AC Q9AUM9:
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DE PUTATIVE SUGAR TRANSPORTER.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Spiegel L.A., King L., Kirchoff K.A., de la Bastide M., Preston R.R.,
RA Nascimento L.U., Vil M.D., Baker J.P., Miller B., Cunniss D.M.,
RA Kuit K.H., Rodriguez S., Santos L., Zutavern T., Ballja V.S.,
RA Shah R.S., Bahret A., Bal H.P., O'Shaughnessy A., Dedhia N.N.,
RA McCombie W.R.
RT "Genomic Sequence for Oryza sativa, Nipponbare Strain, Chromosome X,
RT Clone OSJNB0058B19, Complete Sequence."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC083945; AAK13147.1; -.
KW Sugar transport.
SQ SEQUENCE 574 AA; 60134 MW; 66042EF434ED05E6 CRC64;

Query Match 19.1%; Score 529; DB 10; Length 574;
Best Local Similarity 27.8%; Pred. No. 3.3e-23;
Matches 150; Conservative 83; Mismatches 192; Indels 114; Gaps 12;

QY 11 CASVSLGGLTFGYELAVISGALLPLQDGLGSLCUEQEFVLGSLGALLASLVGGFLID 70
Db 86 CSIGSIISVLNGYDTGVMSGAMLFKEDLKTNDTQOVVLGILNVLCALVGSLSLAGRVS 145
QY 71 CVGRKQAILGSLNVLGSLTGLAGSLAWLVGLRAVVGFAISLSSMACCIIVSELVGR 130
Db 146 CVGRRLTISLAACIFVLGSLVLMGAPNATLILAGRCVAGVGVGVMIAVPTAAETASAD 205
QY 131 ORGVLSVLYEAGITVIGLLSYALNALAGTP--WGWRRHMFGNATAPVLQSLSLFLPAG 188
Db 206 IRGSLTSLPEICISGILIGYVANYLLAKPLVYGVHAWLGLALPASAALCVLAMPES 265
QY 189 -----TDETATHKDLIPLOG-----GEAPKLGPRPRYSFL 219
Db 266 PRWLVVOGRAEALSRLRVCDRPSEADARLAEIKAAAGLADDDGAAANAGSG-CKGVWR 324
QY 220 DLF-RARDNMGRRTTVGLGLVLFQOLTGPQNVLCYASTIFFSVGPHGSSAVLASVGLCA 278
Db 325 ELFLHPTPPVRRIVYTAALGIHFFOHLTGIEAVLYSPRIFKAAGIASRNSVLAAATIGV 384
QY 279 VKVAATLTAMGLVDRAGRALLLACCALMALSVSGIGLVSPAVPMDSGPSCLAVPNATGO 338
Db 385 TKTAFILAILLVDRIGRRPYLS-----SLAGI-TASLA-----CLGMDG----- 423
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QY 339 TGLPGDSSLQDSSLPPIPTNEDQREPIILSTAKKTKPHRSGDPSAPPRALSSALPCP 398
Db 424 -----LTVIERSPPHHS----- 435
QY 399 PLPARGHALLRWTTALLCL--MVFSAFSGFGPVTWLVLSIYVPEIRGAFACNSFN 455
Db 436 --PA-----NAVLAITATVTFVASFSIGVGPITWAYSEVYPLRLRQAQASGVGAIN 486
QY 456 WAANLFLISLFDLIGTIGLSWTFLYGLTAVLGLGFIYFLYFETKGSALAEIDQFOK 514
Db 487 RVMNAGVSMFTVSLKYKAITIGCAFFLEAGLAVAAATFFYLLCPEQTQGRPLEEIEVFSQ 545

RESULT 11
Q9LKH2 PRELIMINARY: PRT: 581 AA.
AC Q9LKH2:
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE PUTATIVE NA+/MYO-INOSITOL SYMPORTER.
GN ITR1.
OS Mesembryanthemum crystallinum (Common ice plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Alzooaceae; Mesembryanthemum.
OX NCBI_TaxID=3544;
RN [1]
RP SEQUENCE FROM N.A.
RA Chauhan S., Forsthoefel N., Ran Y., Quigley F., Nelson D.E.,
RA Bonhert H.J.;
RT "Na+/myo-inositol symporters and Na+/H+-antiporters in plant sodium
RT transport."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
DR EMBL: AF280431; AAF91431.1; -.
DR InterPro: IPR000566; Lipocin_cytfABP.
DR InterPro: IPR001991; Na_dicarboxyl_syp.
DR InterPro: IPR003662; sub_transporter.
DR InterPro: IPR003663; Sugar_transporter.
DR Pfam: PF00083; sugar_tr_1.
DR PRINTS: PR00173; EDTRNSPORT.
DR PRINTS: PR00171; SUGTRNSPORT.
DR PROSITE: PS00213; LIPOCALIN; UNKNOWN_1.
DR PROSITE: PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
DR PROSITE: PS00217; SUGAR_TRANSPORT_2; 1.
KW Transmembrane.
SQ SEQUENCE 581 AA; 62474 MW; EB7EBE1C36D46F1F CRC64;

Query Match 19.1%; Score 529; DB 10; Length 581;
Best Local Similarity 27.6%; Pred. No. 3.4e-23;
Matches 158; Conservative 98; Mismatches 225; Indels 92; Gaps 13;

QY 1 MGHSPVPVPLCASVSLGGLTFGYELAVISGALLPLQDGLGSLCUEQEFVLGSLGALL 57
Db 21 VGTTPVIMRLAFSAG-IGGLFGYDTGVISGALLYTKEDFKEVAQKTLQETIVAMAVAG 79
QY 58 ALLASLVGGFLIDCYGRKQAILGSLNVLGSLTGLAGSLAWLVGLRAVVGFAISLSM 117
Db 80 AIVGAGLGGLNDKFKRPAMIVADILFTGAIIMSVAPAPWIIIGRIWVGVLGVMASM 139
QY 118 ACCIYVSELVGRQGRVLSVLYEAGITVIGLLSYALNALAGTPWGWRRHMFGNATAPVL 177
Db 140 TAPLYISETSPAKIRGALCATNGLITGGQFVSYLVNLGFTRVKGTWRHMLGVAAPAAI 199
QY 178 QSLSLFLPAG-----TDETATHKDLIPLOGEAPKLGPR 211
Db 200 QVVLMLTLPESPRWLYRONKISEAEIILGRIYPPQVKEEDSLKTSIENENADRKAUGE 259
QY 212 GRPRYSFLDLFPARDN--MRGRTTVGLGLVLFQOLTGPQNVLCYASTIFFSVSGHGGSSA 269
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Db 260 GN--AFVRAKRAWDNKNVRRGLIAGISVLVAQGFVGINVTMYSPITIIQAGFASNSTA 316  
 QY 270 VLASVGLGAVKVAATITAMGLVDRAGRALLLA-----GCALMALSVS 312  
 Db 317 LALSIVTSGNAVGSIVSMWFDRGRRRLIISMFATITCLVLSGLFYGAQAAPKIS 376  
 QY 313 GIGLVFAVPMDSGSPCLAVPNATG-----QTGL-PCDGLLQDSSLPPIPTNEDQRE 365  
 Db 377 QLESSHFG-----ANSTCPAFASATSPDRWNCMTCLKASDCAFCSNSASEPHPCACVAQTS 432  
 QY 366 PILSTAKTKPHRPSGDPSAPPLALSSALPGPPLPARGHALLRWTTALLCLMVFVSASF 425  
 Db 433 TMNACLGK-----RIYTECCP-----SKFGEMIIIVGLVITYS 471  
 QY 426 GFPGVTWLVSEIYPVEIRGAFACNSFN-----WAANLFLSLSFLLDGLTIGLSWTFLL 481  
 Db 472 GMGTVPWILNSEIYPLRYRG-----ICGGTAVTLKCANLIVSETFLTLTEALGSGTFL 527  
 QY 482 YGLTAVILGGLFYILFVPETKSGSLAEIDQFOK 514  
 Db 528 YAGFSLIGLIVIFLLVPETKGLPIEDIERMLEK 560

RESULT 12  
 Q9LKH1 ID Q9LKH1 PRELIMINARY; PRT; 581 AA.  
 AC Q9LKH1;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE PUTATIVE Na+/MgO-INOSITOL SYMPORTER.  
 GN ITR2.  
 OS Mesembryanthemum crystallinum (Common ice plant).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Alzooceae; Mesembryanthemum.  
 OX NCBI\_TaxID=3544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Chauhan S., Forsthoefel N., Ran Y., Quigley F., Nelson D.E.,  
 RA Bohnert H.J.;  
 RT "Na+/myo-inositol symporters and Na+/H+-antiporters in plant sodium  
 RT transport.";  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.  
 DR EMBL; AF280432; AAF91432.1; -;  
 DR InterPro; IPR000566; Lipocln\_cytfabp.  
 DR InterPro; IPR001991; Na\_dicarboxyl\_sym.  
 DR InterPro; IPR003662; sub\_transporter.  
 DR InterPro; IPR003663; Sugar\_transporter.  
 DR Pfam; PF00083; sugar\_tr; 1.  
 DR PRINTS; PR00173; EDTRNSPORT.  
 DR PRINTS; PR00171; SUGRTRNSPORT.  
 DR PROSITE; PS00213; LIPOCALIN; UNKNOWN\_1.  
 DR PROSITE; PS00217; SUGAR\_TRANSPORT\_2; 1.  
 KW Transmembrane.  
 SQ SEQUENCE 581 AA; 62818 MW; 5C8F9A150FBFA5FF CRC64;

Query Match 19.0%; Score 526.5; DB 10; Length 581;  
 Best Local Similarity 28.6%; Pred. No. 4.7e-23;  
 Matches 164; Conservative 86; Mismatches 229; Indels 95; Gaps 12;

QY 1 MGHSPVPLPCASVLLGLTFGYELAVISGALLPLQDF---GLSCLEQEFVLSLLG 57  
 Db 21 IGKTYILRLAFASAG-IGGLFGYDTGVISGALLIKEDFEVERKTKLQETIVAMAVAG 79  
 QY 58 ALLASLVGGFLDCYGRKQATILGSNLVLGASLTILGAGSLANVLGRVAVGFAISLSM 117  
 Db 80 ALIAGVGGLNDKRGKPAIIADIIFIGAITMSLAPWMLILGRIFVGLGVGMAS 139  
 QY 118 ACCIYVSELVGRGVLVLYEAGITVIGILLSVALNYALAGTPWGRHRMFGWATAPAVL 177

Db 140 TSPLYISESPTRIRSAVSTNGLLITGSQFLSYLINLGFTRVKGTWRMMLGVAAPAFV 199  
 QY 178 QSLSLFLPLPAG-----TDETATHKDLIPLQCGEAPKLGP 211  
 Db 200 QLLMLSLPESPRWLYRKKNVVEAEAILARIYPPVEEEMRAKASIEYEMAEIGEIG 259  
 QY 212 GRPRYSFLDLFR---ARDNWRGRTTVGLGLVLPQQLTGOPNVLCYASTIFSSVGFHGGSS 268  
 Db 260 G-----SMLSKVRKAMGNKIVRRGLYAGITVOVAQFVGINTVMYSPITVQLAGFASNST 315  
 QY 269 AVLASVGLGAVKVAATLTAMGLVDRAGRALLAGCALMALSVSGIGLVSAFVPMDSGSPS 328  
 Db 316 ALALSIVTSGLNAIGSIVSMFVDRHGRRLMI-----ISMFGII-----T 356  
 QY 329 CLAVPNATGOTGLPGDGLLQDSSLPPIPTNEDQREPIILST--AKTKPHRPSGDPSAP 386  
 Db 357 CLIVLAI-----GFFQAAAHAPKISHAESTHFGNLSTCPAYTTTRNPNATWNCMT 406  
 QY 387 PRLALSSA-----LPG-----PPLPARGHALLRWTT-----ALLCLMVF 419  
 Db 407 LQAASECAFTKNGNQLLPGCVSRDAMKVACHGKRYFTFGCPKSGFGLAVILLGAY 466  
 QY 420 VSAFSGFGPVTWLVSEIYPVEIRGAFACNSFNAAANLFLSLSFLLDGLTIGLSWTF 479  
 Db 467 IISYSPGMGTVPWIVNSEIYPLRYRGVGGIAAVSNWTSNLIVSEFTLTLTEALGAAGTF 526  
 QY 480 LLYGTVAVILGGLFYILFVPETKSGSLAEIDQFOQ 513  
 Db 527 LLFAGFSAIGLVFIYLLVPETKGLPIEEVEHMLE 560

RESULT 13  
 Q9CFH3 ID Q9CFH3 PRELIMINARY; PRT; 433 AA.  
 AC Q9CFH3;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE D-XULOSE PROTON-SYMPORTER.  
 GN XULT.  
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
 OC Lactococcus.  
 OX NCBI\_TaxID=1360;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ILL403;  
 RA Boletín A., Wincker P., Mauger S., Jaillon O., Malarne K.,  
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;  
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus  
 RT lactis.";  
 RL Genome Res. 0:0-0(2001).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.  
 DR EMBL; AE006381; AAK05601.1; -;  
 DR InterPro; IPR003662; sub\_transporter.  
 DR InterPro; IPR003663; Sugar\_transporter.  
 DR Pfam; PF00083; sugar\_tr; 1.  
 DR PRINTS; PR00171; SUGRTRNSPORT.  
 DR PROSITE; PS00216; SUGAR\_TRANSPORT\_1; 1.  
 KW Complete proteome; Transmembrane.  
 SQ SEQUENCE 433 AA; 46868 MW; A57BF50C4ABE70A0 CRC64;

Query Match 18.9%; Score 521.5; DB 2; Length 433;  
 Best Local Similarity 28.9%; Pred. No. 6.7e-23;  
 Matches 146; Conservative 79; Mismatches 158; Indels 123; Gaps 11;  
 QY 17 LGGITFCYELAVISGALLPLQDFGLSCLEQ-----FLVGSLLIGALLASLV 64  
 Db 15 LGGLLFGYDTGVISGALL-----FIEKSNQVSSWANNMEGWITAALMGAVIGAV 65



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QY 65 GGFLIDCYGRKQAILGSLNVLGAGSLTGLAGSLAWLVLGRAVGFATLSLSSMACCIYVS 124
DB 66 ICPMSDRFGRKRLLLLSLAFVFFVAGLGSLSNSALIIISRVILGMVGSASALVPTLYLS 125
QY 125 ELVGPRQGVLSVLYEAGITVCGILLISYALNYALAGTTPMGRHMFWMGATAPAVLQSLSLIF 184
DB 126 ELSPAKIRGVSTPMQIMTGLLAYSIALYALKVSGNWHMGLGATVPAALLFIGGLF 185
QY 185 LPAGTDETHAKDLPLQGGAPKLG-----PGRPRYSFLDL-FRARDNMGR----- 231
DB 186 LPESPRFLVRHON-----EAGAREILLGMINDPNSTAEISDQLMAKEKOGGLOELFQ 241
QY 232 -----TTVGLGLVLFQOLTGPVNLVLYASTIFSSVCGHGSASVAVLGLGAVKVAATLT 286
DB 242 MBRPVLIMAGLAIFQVGVGNTVLYFAPSIFVAVGF-GASAAALLAHIGIFNVIVTVI 300
QY 287 ANGLVDRAGRALLAGCALMALSVSGIGLVAFVPMDSGSPCLAVPNATGOTGLPGDSG 346
DB 301 ANRVMDKVNRRMLNFGWGM-----GISVLMSVGM-----ILAENA----- 338
QY 347 LQDSSLPPIPTNEDQREPILSTAKTKPHPRSGDPSAPPRLALSSALPGPPLPARGHA 406
DB 339 -----HIGFG----- 343
QY 407 LLRWLTALLCLMVFSAFSGFPGVTWLVLSLSEIYPVEIRGAFACFNSFNMAANLFISSLF 466
DB 344 ---KYLAVALTATVYIAFFSATWGPVMVMYIGESFPLKIRGLGNSFGAANVMAANVVSILTF 401
QY 467 LDLICTIGLSWTFLLYGLTAVLGLGF 492
DB 402 LPLLSFFGTGKIFLIYACCFLSINP 427

RESULT 14
Q9LLE1 PRELIMINARY; PRT; 534 AA.
AC Q9LLE1;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DE 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE HEXOSE TRANSPORTER (FRAGMENT).
GN PGCT.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN 11;
RP SEQUENCE FROM N.A. PubMed=10810150;
RX MEDLINE=2021774; Geiger D.R., Kofler H., Hille D., Groner F.,
RA Weber A., Servaites J.C., Flügge U.I.;
RT "Identification, Purification, and Molecular Cloning of a Putative
RT Plastidic Glucose Translocator.";
RL Plant Cell 12:787-802(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
DR EMBL; AF215852; AAF74565.1;
DR InterPro; IPR003662; sub_transporter.
DR Pfam; PF00083; sugar_tr; 1.
DR PRINTS; PR00171; SUGRTRNSPORT.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
FT NON_TER 1
SQ SEQUENCE 534 AA; 56482 MW; 676A5E6C3C809ECA CRC64;

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Query Match 18.8%; Score 519; DB 10; Length 534;  
 Best Local Similarity 30.0%; Pred. No. 1.2e-22;  
 Matches 158; Conservative 75; Mismatches 188; Indels 106; Gaps 12;

QY 4 SPVPLPLCASVSLGLTFGYELAVISGALLPLQLDFGL--SCLRQEFVLVGSLLIGALLA 61

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DB 90 SGSVLPY-VGVACLAGLPGYHLGVVNGALEYLAQDLGIVENTVTOGWIVSVVLACATVG 148
QY 62 SLVGGFLIDCYGRKQAILGSLNVLGAGSLTGLAGSLAWLVLGRAVGFATLSLSSMACCI 121
DB 149 SFTGGALADKFGRTKFTVLDLAIPAVGAPLCTTAQSVQAMIIIGRLLTGIGISSAIVPL 208
QY 122 YVSELVGPQRGVLSVLYEAGITVCGILLISYALNYALAGTTPMGRHMFWMGATAPAVLQ 181
DB 209 YISEISPTIEIRGLTGTNQLFICIGILVALVAGLPLSGNPLMWRMTMFGIALIPSVLLAIG 268
QY 182 LLFLPAG-----TDETATH-----KDLIPLQGG--EAPKLGPRPRYSFLDLFRA 224
DB 269 MAFSPESPRMLFQQRISAEATSIKRLYCKERVAEVMGDLASAQSSSEPDAGNLDLFS 328
QY 225 RDNMRGRTTVGLVGLVLFQOLTGPVNLVLYASTIFSSVCGHGSASVAVLGLGAVKVAAT 284
DB 329 R--YKWKVVSIGAAALFLFOQFAGINAVVYSTAVERSAGI---SSDVAASALYCAANVFCT 383
QY 285 LTAMGLVDRAGRALLAGCALMALSVSGIGLVAFVPMDSGSPCLAVPNATGOTGLPGD 344
DB 384 MYASLMDKQGRKSL-----LVSF-----TCMAAS 409
QY 345 SGLQDSSLPPIPTNEDQREPILSTAKTKPHPRSGDPSAPPRLALSSALPGPPLPARG 404
DB 410 MMLLS-----LSFTWKVLT-PYSGT----- 428
QY 405 HALLRWLTALLCLMVFSAFSGFPGVTWLVLSLSEIYPVEIRGAFACFNSFNMAANLFI 464
DB 429 -----LAVLGTVLYVLSFSLGAGVPVALLPEIFASIRAKRAVALSLGHHWISNFFIGL 482
QY 465 SFLDLIGTIGLSWTFLLYGLTAVLGLGFYLFVPEYKSGOSLAIDQO 511
DB 483 YFLSVITKFGISTVYLGFAVCVCLLAVMVIYGVNVTGKRSLEDIERE 529

RESULT 15
Q9LLE0 PRELIMINARY; PRT; 470 AA.
AC Q9LLE0;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DE 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE HEXOSE TRANSPORTER (FRAGMENT).
GN PGCT.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN 11;
RP SEQUENCE FROM N.A. PubMed=10810150;
RX MEDLINE=2021774; Geiger D.R., Kofler H., Hille D., Groner F.,
RA Weber A., Servaites J.C., Flügge U.I.;
RT "Identification, Purification, and Molecular Cloning of a Putative
RT Plastidic Glucose Translocator.";
RL Plant Cell 12:787-802(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: TO SUGAR TRANSPORTER FAMILY.
DR EMBL; AF215853; AAF74567.1;
DR InterPro; IPR003662; sub_transporter.
DR Pfam; PF00083; sugar_tr; 1.
DR PRINTS; PR00171; SUGRTRNSPORT.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
FT NON_TER 1
SQ SEQUENCE 470 AA; 49667 MW; FC11D804C93ED71 CRC64;

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Query Match 18.7%; Score 516; DB 10; Length 470;  
 Best Local Similarity 28.8%; Pred. No. 1.5e-22;

Search completed: March 15, 2002, 07:09:18  
Job time: 329 sec